Workshop on Nonlinear and Topological Methods in Biomedical Signal Analysis
Gdańsk University of Technology, November 26–27, 2025

Inferring Higher-Order Hidden drivers from fMRI Data

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joint work with Zsigmond Benkő[1], Marcell Stippinger[1], Asadur Chowdury[2], David R. Rosenberg[2], Vaibhav A. Diwadkar[2]

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Traditional approaches to analyzing interactions between brain areas have primarily focused on networks built from pairwise relationships between measured activities. These include functional connectivity, typically quantified using correlation, and causality analyses, which aim to infer directional couplings between regions of interest. Only a few studies have attempted to infer the emergence of higher-order interactions between brain areas using multivariate extensions of entropy-based measures, such as Mutual Information, Total Correlation, Dual Total Correlation, or topological invariants. While these measures capture important aspects of information processing in the brain, some of their mathematical properties – such as the potential negativity of higher-order Mutual Information – limit their interpretability.

Here, we introduce a novel method to infer the dimensionality of higher-order hidden drivers based on multiple time series from dynamical systems. We prove the non-negativity of the interaction dimension analytically and validate our inference algorithm on simulated networks of dynamical systems. We then apply the method to fMRI time series data to investigate the existence and complexity of hidden common drivers among eight brain regions associated with visuomotor responding and working memory tasks. We find evidence of significant task-specific differences in higher-order driver structures, both in the involvement of specific groups of brain areas and in the typical order of the significant drivers.

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Dimensional causality and hidden drivers in cardiovascular and respiratory time series

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Cardiovascular and pulmonary diseases often arise from disturbances in the interactions among heart rate, blood pressure, and respiratory dynamics. In this study, we analyze parallel recordings of respiratory signals, ECG, and instantaneous blood pressure to uncover the underlying regulatory architecture.

We apply a topological framework based on Takens' embedding theorem to reconstruct the joint state-space dynamics of these signals and to characterize interactions between subsystems using observation-only data. The presence of multiple feedback loops poses a fundamental challenge in complex systems analysis.

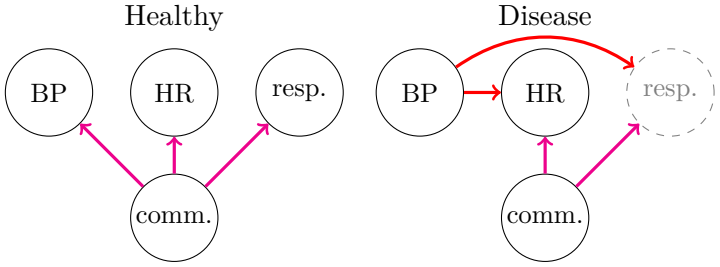
First, we introduce a novel method called Dimensional Causality (DC), which uniquely distinguishes all fundamental causal relationships between two subsystems: unidirectional causality, bidirectional interactions, hidden common causes, and independence. DC estimates the intrinsic dimension of the reconstructed state space and applies Bayesian inference to assign probabilities to competing causal structures. In comparative evaluations on simulated systems with known ground truth, DC consistently outperformed state-of-the-art methods, even under optimized conditions [1].

Our goal is to quantify the direction and strength of causal influences between cardiovascular and respiratory signals under resting conditions, both

in healthy individuals and in patients with cardiovascular disease, with particular emphasis on hypertension.

We observe that the dimension of the respiratory dynamics changes significantly between the two groups. The dimension of respiration decreases in individuals with disease, and in parallel, the joint dimension of respiration/blood pressure (BP) and respiration/heart rate (HR) also decreases.

In the disease group, these dimensional changes alter the inferred causal relationships from a hidden common cause connecting the subsystems to cardiovascular signals (BP, HR) driving respiration.



In our interpretation, there is a hidden common cause that affects breathing, heart rate (HR), and blood pressure (BP). In the healthy case, all three are affected by other factors or possess their own intrinsic dynamics with degrees of freedom, which leads to the conclusion of a hidden common cause. However, in the diseased group, the other effects influencing blood pressure weaken, or the degrees of freedom in its intrinsic dynamics diminish. As a result, blood pressure becomes synchronized with the hidden common cause, becoming a direct driver of breathing and heart rate. It is also possible that blood pressure itself becomes the driver of both heart rate and respiration, effectively acting as their common cause. The observed decrease in the dimension of respiration requires further investigation.

Finally, we further analyze the joint dimensions to reveal the structure of pairwise hidden common causes or the existence of a higher-order hidden common cause.

Our dimensional approach has the potential to identify early markers of cardiovascular dysfunction, improve diagnostic algorithms for altered autonomic regulation, and deepen our understanding of physiological dynamics.

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Integrative Exploration of Cardiorespiratory Interactions: An Interdisciplinary Study

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Cardiorespiratory interaction refers to the complex and dynamic interplay between the cardiovascular and the respiratory systems. This interaction is essential for maintaining homeostasis and optimizing the body's responses to various internal and external stimuli. Disorders that affect either the heart or lungs can disrupt this crucial relation. For example, heart failure can impair the ability of the heart to pump effectively, which can lead to inadequate oxygen delivery and respiratory distress. Conversely, pulmonary diseases can lead to impaired gas exchange and increased cardiac workload.

Studying interactions, especially their impact on heart rate dynamics, is essential to understand the mechanisms of cardiovascular abnormalities and crucial for better prevention, diagnosis and management of diseases that comprise respiratory, cardiovascular and autonomic nervous systems.

However, most of the known cardiorespiratory interactions require further investigation. The results of current research mainly concern healthy individuals and little is known about changes of interactions at the initial stage of cardiovascular disease. There is particularly not enough data on this topic when the respiratory pattern is irregular or changes over time.

The talk will present our study on the role of alterations in breathing patterns in cardiovascular disease. The study design, including its interdisciplinary approach, as well as results from both human and animal studies, will be discussed.

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Detecting topological conjugacy of dynamical systems via TDA

Justyna Signerska-Rynkowska[1]

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In the talk I will show how to bring TDA type invariants to dynamical data. In particular, I will present topology-based statistical tests for verifying (semi-)conjugacy of discrete dynamical systems, which provide a framework to study equivalence of dynamics under noise and embedding transformations. The tests work directly on sampled trajectories and therefore no explicit model reconstruction is needed. The methods are exemplified on synthetic benchmark data generated by a rotation map on the Klein bottle, the Lorenz system, tent and logistic maps. However, potential applications include detecting equivalence of biological, physical, or financial systems from time series as well as model validation for reconstructed or data-driven dynamical systems.

I will also mention a recently developed tool based on Euler Characteristic Profiles for detecting conjugacy of continuous dynamical systems which opens a new way for investigating biological and physical data in the form of vector fields (such as gene migration data or ocean currents).

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[2] P. Dłotko, M. Marszewska, J. Signerska-Rynkowska. Topological characteristics of dynamics: New stable characteristics on discrete and continuous dynamical systems. (in preparation) (2025)

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Recurrence Method in the Analysis of Electroencephalographic Signals in Healthy Adults under Light-Dark Conditions.

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Electroencephalography is one of the non-invasive techniques used for analyzing brain activity. Its signals are recorded from several electrodes placed on the scalp. Recorded signals reflect the functional state of the brain, which is allied to the person's mental condition.

We analyze electroencephalographic signals (EEG signals) using recurrence methods. These signals were collected during an experiment where each person was exposed to light of two different colors (blue and red) in contrast to the dark. In addition to linear signal filtering methods and independent component analysis applied to EEG signals, we used a non-linear method, recurrence plot, to characterize the system that produces them.

Using Takens theorem, we obtain a set of vectors that were built from the value of the EEG signals. Then we analyze the distance matrix between vectors obtained from the one chosen EEG signal. Based on these matrices we perform recurrence quantification analysis, and calculate: percent determinism, Shannon entropy and average line length. They gives information about changes in the dynamics of the sources producing the EEG signal under light-dark conditions. We demonstrate that light selectively affects EEG signal sources. Their effects are also diversed by changes in the dynamic properties of these sources.

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From Tissue Damage to Lost Beats: Modeling Infarction in the SAN

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A cellular automaton model reproduces the microstructure and bioelectric conduction within the sinoatrial node (SAN), incorporating cellular heterogeneity (cardiomyocytes, fibroblasts, collagen) and the presence of connexins (Cx43, Cx45, Cx40). The model simulates infarction which is related ischemia in the SAN head as a growing gradient of biochemical and electrical disturbances, leading to connexin degradation and altered cellular properties.

The results show that the progression of ischemia leads to conduction abnormalities, interruption of the signal transmitted to the atria, and activation of an escape rhythm originating from the AV node. The model also reveals phenomena not previously described in the context of the SAN.

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A Conceptual Outlook on Gene Migration Analysis Using an Euler-Based Method

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joint work with Justyna Signerska-Rynkowska[2], Paweł Dłotko[3], and Michael Bleher[4]

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Euler Characteristic Profiles (ECPs) [1] have recently gained attention within topological data analysis as a compact and computationally tractable descriptor of high-dimensional dynamical systems. In this talk, I outline an initial conceptual idea for applying ECPs to datasets related to gene migration and the movement of genetic information across populations. Rather than presenting definitive results, the aim is to discuss a possible framework in which population-level genetic variation is treated as a dynamic topological object whose evolving structure might be probed through ECP-based methods. Such an approach could, in principle, provide complementary perspectives on changes in genetic composition. The talk will therefore focus on the motivation, the theoretical rationale, and the open questions surrounding the adaptation of ECPs to population-genetic settings, with an emphasis on identifying potential challenges and directions for future investigation.

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Analysis of the Chaotic Itinerancy Phenomenon using Entropy and Clustering

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joint work with Paweł Pilarczyk[1]

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Chaotic itinerancy is a type of behavior observed in dynamical systems situated at the boundary between chaos and order. In this phenomenon, a trajectory is attracted to an ordered motion state and stays there for a while. Then, it departs from the ordered motion state and enters into high-dimensional chaotic motion. After some time, the trajectory returns to a different (or possibly the same) ordered state, and this process continues. Such ordered states are called attractor ruins, as they appear to originate from attractors that lost their stability due to bifurcation. The system's trajectory wanders unpredictably among these attractor ruins. Chaotic itinerancy is applied in diverse contexts, including the modeling of brain activity [1] and the simulation of spontaneity in artificial intelligence [2].

In this talk, I will present a method for detecting the chaotic itinerancy phenomenon based on machine learning and statistical measures of uncertainty [3]. I will demonstrate this method on a system of globally coupled logistic maps, which is a well-known example in the literature [1]. The use of the concept of entropy enables the identification of parameter ranges in which chaotic itinerancy can be observed. Applying a clustering algorithm to the trajectory points in phase space allows for the detection of dense regions as potential approximations of attractor ruins. For such identified clusters, transitions between them can be analyzed, and statistical tests of randomness can be performed to confirm the unpredictability of the dynamics, which is a key feature of this phenomenon.

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Classification of ECG signals through persistent homology

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The algorithmic analysis of ECG signals is a non-trivial task due to the variety and complexity of cardiac abnormalities reflected in heart-rate dynamics. In this work, we investigate a topological approach to ECG classification. Topological Data Analysis (TDA) has recently emerged as a effective framework for problems in which the topology and geometric structure of the data serves as an descriptor of the underlying phenomenon. The main tool in TDA is persistent homology, which allows to capture spacial structure of the data, e.g. number of connected components, cycles, and n-dimensional voids across many scales. We propose an algorithmic pipeline for binary classification of ECG signals that incorporates Takens' embedding to encode time-series data as a point clouds in $\mathbb{R}^n$, followed by dimensionality reduction using PCA to enable efficient computation of persistence diagrams and their vectorizations. We evaluate the performance of random forest classifiers trained on: (i) raw ECG signals, (ii) TDA features, and (iii) raw signals augmented with TDA features. Our results demonstrate the potential of topological descriptors to enhance classification performance for certain types of time-series data.

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Topological-numerical analysis of the discrete-time two-gene Andrecut-Kauffman model

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We analyze the behavior of a gene expression model first introduced by Andrecut and Kauffman [1]. We identify chaotic and ordered dynamics using maximal Lyapunov exponent and perform numerical simulations for a wide range of parameters. We find parameter values resulting in the presence of multiple attractors, which have the potential for representing real-world phenomena [2]. Moreover, we obtain Morse decomposition of the system by utilizing a rigorous numerical algorithm. We compute isolating neighborhoods of attractors as well as unstable sets, providing a birds-eye view of the dynamics present in the system. We gain further insight into the model by computing Conley indices for the isolating neighborhoods, which are visualized using comprehensive Conley-Morse graphs. Our results showcase the utility of topological methods in analyzing complex biological systems and their advantages over simpler numerical simulations.

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